

CLAIMS

What is claimed is:

1. An isolated polynucleotide comprising a first nucleotide sequence encoding a polypeptide of at least 112 amino acids that has at least 80% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:4, 6, 14, 24, 32, 34, 36, 38, 42 and 44, or a second nucleotide sequence comprising the complement of the first nucleotide sequence.
2. The isolated polynucleotide of Claim 1, wherein the first nucleotide sequence consists of a nucleic acid sequence selected from the group consisting of SEQ ID NOs:3, 5, 13, 23, 31, 33, 35, 37, 41 and 43 that codes for the polypeptide selected from the group consisting of SEQ ID NOs:4, 6, 14, 24, 32, 34, 36, 38, 42 and 44.
3. The isolated polynucleotide of Claim 1 wherein the nucleotide sequences are DNA.
4. The isolated polynucleotide of Claim 1 wherein the nucleotide sequences are RNA.
5. A chimeric gene comprising the isolated polynucleotide of Claim 1 operably linked to suitable regulatory sequences.
6. An isolated host cell comprising the chimeric gene of Claim 5.
7. A host cell comprising an isolated polynucleotide of Claim 1.
8. The host cell of Claim 7 wherein the host cell is selected from the group consisting of yeast, bacteria, plant, and virus.
9. A virus comprising the isolated polynucleotide of Claim 1.
10. A polypeptide of at least 112 amino acids that has at least 80% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:4, 6, 14, 24, 32, 34, 36, 38, 42 and 44.
11. An isolated polynucleotide comprising a first nucleotide sequence encoding a polypeptide of at least 163 amino acids that has at least 80% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:12, 28 and 40, or a second nucleotide sequence comprising the complement of the first nucleotide sequence.
12. The isolated polynucleotide of Claim 11, wherein the first nucleotide sequence consists of a nucleic acid sequence selected from the group consisting of SEQ ID NOs:11, 27 and 39 that codes for the polypeptide selected from the group consisting of SEQ ID NOs:12, 28 and 40.
13. The isolated polynucleotide of Claim 11 wherein the nucleotide sequences are DNA.
14. The isolated polynucleotide of Claim 11 wherein the nucleotide sequences are RNA.

15. A chimeric gene comprising the isolated polynucleotide of Claim 11 operably linked to suitable regulatory sequences.

16. An isolated host cell comprising the chimeric gene of Claim 15.

17. A host cell comprising an isolated polynucleotide of Claim 11.

18. The host cell of Claim 17 wherein the host cell is selected from the group consisting of yeast, bacteria, plant, and virus.

19. A virus comprising the isolated polynucleotide of Claim 11.

20. A polypeptide of at least 163 amino acids that has at least 80% identity based on the Clustal method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOs:10, 20 and 40.

21. A method of selecting an isolated polynucleotide that affects the level of expression of a polyphenol oxidase enzyme polypeptide in a plant cell, the method comprising the steps of:

(a) constructing an isolated polynucleotide comprising a nucleotide sequence of at least one of 30 contiguous nucleotides derived from an isolated polynucleotide of any of Claims 1 or 11;

(b) introducing the isolated polynucleotide into a plant cell;

(c) measuring the level of a polypeptide in the plant cell containing the polynucleotide; and

(d) comparing the level of polypeptide in the plant cell containing the isolated polynucleotide with the level of polypeptide in a plant cell that does not contain the isolated polynucleotide.

22. The method of Claim 21 wherein the isolated polynucleotide consists of a nucleotide sequence selected from the group consisting of SEQ ID NOs:3, 5, 11, 13, 23, 27, 31, 33, 35, 37, 39, 41 and 43 that codes for the polypeptide selected from the group consisting of SEQ ID NOs:4, 6, 12, 14, 24, 28, 32, 34, 36, 38, 40, 42 and 44.

23. A method of selecting an isolated polynucleotide that affects the level of expression of a polyphenol oxidase enzyme polypeptide in a plant cell, the method comprising the steps of:

(a) constructing an isolated polynucleotide of any of Claims 1 or 11;

(b) introducing the isolated polynucleotide into a plant cell;

(c) measuring the level of polypeptide in the plant cell containing the polynucleotide; and

(d) comparing the level of polypeptide in the plant cell containing the isolated polynucleotide with the level of polypeptide in a plant cell that does not contain the polynucleotide.

24. A method of obtaining a nucleic acid fragment encoding a polyphenol oxidase enzyme polypeptide comprising the steps of:

(a) synthesizing an oligonucleotide primer comprising a nucleotide sequence of at least one of 30 contiguous nucleotides derived from a nucleotide sequence selected from the group consisting of SEQ ID NOs:3, 5, 11, 13, 23, 27, 31, 33, 35, 37, 39, 41 and 43 and the complement of such nucleotide sequences; and

5 (b) amplifying a nucleic acid sequence using the oligonucleotide primer.

25. A method of obtaining a nucleic acid fragment encoding a polyphenol oxidase enzyme polypeptide comprising the steps of:

(a) probing a cDNA or genomic library with an isolated polynucleotide comprising at least one of 30 contiguous nucleotides derived from a nucleotide sequence selected from the group consisting of SEQ ID NOs:3, 5, 11, 13, 23, 27, 31, 33, 35, 37, 39, 41 and 43 and the complement of such nucleotide sequences;

(b) identifying a DNA clone that hybridizes with the isolated polynucleotide;

(c) isolating the identified DNA clone; and

(d) sequencing the cDNA or genomic fragment that comprises the isolated DNA clone.

26. A composition comprising the isolated polynucleotide of any of Claim 1 or 11.

27. A composition comprising the isolated polypeptide of any of Claims 10 or 20.

28. An isolated polynucleotide comprising the nucleotide sequence having at least one of 30 contiguous nucleotides derived from a nucleic acid sequence selected from the group consisting of SEQ ID NOs:3, 5, 11, 13, 23, 27, 31, 33, 35, 37, 39, 41 and 43 and the complement of such sequences.

29. An expression cassette comprising an isolated polynucleotide of any of Claims 1 or 11 operably linked to a promoter.

30. A method for positive selection of a transformed cell comprising:

(a) transforming a host cell with the chimeric gene of any of Claims 5 or 15; and
(b) growing the transformed host cell under conditions which allow expression of the polynucleotide in an amount sufficient to complement a null mutant to provide a positive selection means.

31. A method for positive selection of a transformed cell comprising:

(a) transforming a host cell with the expression cassette of Claim 29; and
(b) growing the transformed host cell under conditions which allow expression of the polynucleotide in an amount sufficient to complement a null mutant to provide a positive selection means.

32. The method of any of Claims 21 or 23 wherein the plant cell is a monocot.

33. The method of any of Claims 21 or 23 wherein the plant cell is a dicot.

34. An isolated polynucleotide comprising a first nucleotide sequence encoding a polypeptide of at least 50 amino acids that has at least 80% identity based on the Clustal

method of alignment when compared to a polypeptide selected from the group consisting of SEQ ID NOS:2, 8, 12, 16, 18, 22, 30 and 46.